OM protein - protein search, using sw model

GenCore version 5.1.6
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Run on: May 25, 2004, 11:07:32 ; Search time 21 Seconds
                                          (without alignments)
                                          82.450 Million cell updates/sec

Title: US-09-847-586-77
Perfect score: 89
Sequence: 1 AKSPVKEEAKSPEKAKSP 18

Scoring table: BLOSUM62
               Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database : PIR 78:*
            1: pir1:*
            2: pir2:*
            3: pir3:*
            4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	DB ID	Description
1	89	100.0	30	2	S02571	neurofilament trip
2	89	100.0	332	2	B43427	neurofilament prot
3	89	100.0	606	2	A43427	neurofilament trip
4	89	100.0	1020	2	QFHUH	neurofilament trip
5	76	85.4	854	2	S02003	neurofilament trip
6	76	85.4	1072	1	A37221	neurofilament trip
7	76	85.4	1087	1	QFMSH	neurofilament trip
8	61	68.5	532	2	QFPGM	neurofilament trip
9	59.5	66.9	916	2	A27864	neurofilament trip
10	56	62.9	20	2	I53671	neurofilament heav
11	52	58.4	942	2	JC7316	neurofilament trip
12	51.5	57.9	6642	2	T29757	protein UNC-89 - C
13	51	57.3	288	2	T06257	histone H1 (clone
14	49	55.1	659	2	B87719	protein R19.5 [lim
15	49	55.1	849	2	S00030	neurofilament trip
16	49	55.1	1200	2	A46194	neurofilament prot
17	48.5	54.5	219	1	HSHU1B	neurofilament trip
18	48	53.9	206	1	HSTR1R	histone H1 - rainb
19	48	53.9	218	1	HSCH1	histone H1 - ch
20	48	53.9	218	2	A23055	histone H1.02 - ch
21	48	53.9	218	2	S01262	histone H1 - musco
22	48	53.9	220	2	A28456	histone H1.01 - ch
23	48	53.9	221	2	S33219	histone H1.C - Afr
24	48	53.9	223	1	S49492	histone H1 - mouse
25	48	53.9	226	1	S16660	histone H1-5 [vali
26	48	53.9	845	2	A45669	neurofilament trip
27	48	53.9	858	2	S15762	neurofilament trip
28	48	53.9	1208	2	T05077	hypothetical prote
29	47.5	53.4	209	1	HSXL1A	histone H1A - Afri
30	47.5	53.4	221	2	S49482	histone H1 - mouse
31	47.5	53.4	229	2	I51227	histone H1A - Afri
32	47.5	53.4	248	1	HSUR1P	histone H1, gonada
33	47	52.8	219	2	C28456	histone H1.11R - c
34	47	52.8	224	2	B28456	histone H1.03 - ch
35	47	52.8	225	2	B28456	methyl-CpG binding
36	47	52.8	476	2	S57963	methyl-CpG-binding
37	47	52.8	492	1	A41907	methyl CpG binding
38	46.5	52.2	219	1	HSXL1B	histone H1B - Afri
39	46.5	52.2	220	1	I51447	histone H1B - Afri
40	46.5	52.2	221	1	B40335	histone H1-3 [vali
41	46.5	52.2	236	2	S22322	histone H1 - wheat
42	46	51.7	212	2	A28470	histone H1 - mouse
43	46	51.7	284	2	T06241	histone H1 (clone
44	46	51.7	1356	2	T16754	hypothetical prote
45	45.5	51.1	196	1	HSXL5A	histone H5A - Afri

ALIGNMENTS

RESULT 1
S02571
neurofilament triplet protein H - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 10-Dec-1999
C;Accession: S02571
R;Geisler, N.; Vandekerckhove, J.; Weber, K.
FEBS Lett. 221, 403-407, 1987
A;Title: Location and sequence characterization of the major phosphorylation sites of the
A;Reference number: S02570; S02571; MUID:87304852; PMID:3114005
A;Accession: S02571
A;Molecule type: protein
A;Residues: 1-30 <GEI>
A;Experimental source: spinal cord
A;Note: 5-Glu, 19-Glu, and 21-Glu were also found
C;Superfamily: neurofilament triplet H protein
C;Keywords: coiled coil; heterodimer; intermediate filament; nerve; phosphoprotein
F;3,17/Binding site: phosphate (Ser) (covalent) #status experimental

Query Match   100.0%; Score 89; DB 2; Length 30;
Best Local Similarity   100.0%; Pred. No. 1.1e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 AKSPVKEEAKSPEKAKSP 18
           ||||||||||||||||||
Db   1 AKSPVKEEAKSPEKAKSP 18

RESULT 2
B43427
neurofilament protein H form H2 (repetitive region) - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 10-Jul-1998
R;Soppet, D.R.; Beasley, L.L.; Willard, M.B.
J. Biol. Chem. 267, 17354-17361, 1992
A;Title: Evidence for unequal crossing over in the evolution of the neurofilament polypep
A;Reference number: A43427; MUID:92381055; PMID:1512270
A;Accession: B43427
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 1-332 <SOP>
A;Experimental source: brain
A;Note: sequence extracted from NCBI backbone (NCBIP:112012)
C;Superfamily: neurofilament triplet H protein

Query Match   100.0%; Score 89; DB 2; Length 332;
Best Local Similarity   100.0%; Pred. No. 1.2e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 AKSPVKEEAKSPEKAKSP 18
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Qy   1 AKSPVKEEAKSPEKAKSP 18

Db   84 AKSPVKEEAKSPEKAKSP 101

RESULT 3
A43427
neurofilament triplet H1 protein - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 10-Dec-1999
C;Accession: A43427
R;Soppet, D.R.; Beasley, L.L.; Willard, M.B.
J. Biol. Chem. 267, 17354-17361, 1992
A;Title: Evidence for unequal crossing over in the evolution of the neurofilament polype
A;Reference number: A43427; MUID:92381055; PMID:1512270
A;Accession: A43427
A;Molecule type: DNA
A;Residues: 1-606 <SOP>
A;Cross-references: GB:M94315; NID:g164990; PIDN:AAA57152.1; PID:g601930
A;Experimental source: brain
A;Note: sequence extracted from NCBI backbone (NCBIN:112010, NCBIP:112011)
C;Superfamily: neurofilament triplet H protein
C;Keywords: coiled coil; heterotrimer; intermediate filament; nerve; phosphoprotein

Qy   Query Match
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      Matches   18; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

         1 AKSPVKEEAKSPEKAKSP 18
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Db   92 AKSPVKEEAKSPEKAKSP 109

RESULT 4
QHFUH
neurofilament triplet H protein - human
N;Alternate names: neurofilament protein, 112K
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 16-Jun-2000
C;Accession: S00979
R;Rees, J.F.; Sheidman, P.S.; Skuntz, S.F.; Carden, M.J.; Lazzarini, R.A.
EMBO J. 7, 1947-1955, 1988
A;Title: The structure and organization of the human heavy neurofilament subunit (NF-H)
A;Reference number: S00979; MUID:88328981; PMID:3138108
A;Accession: S00979
A;Molecule type: DNA
A;Residues: 1-1020 <LEE>
A;Cross-references: EMBL:X15306; NID:g35028; PIDN:CAA33366.1; PID:g1841430
A;Note: it is uncertain whether Met-1 or Met-2 is the initiator
C;Genetics:
A;Gene: GDB:NEFH
C;Cross-references: GDB:120025; OMIM:162230
A;Map position: 22q12.;-22q13.1
A;Introns: 295/1; 361/3; 403/2
C;Status: preliminary
C;Superfamily: neurofilament triplet H protein
C;Keywords: coiled coil; heterotrimer; intermediate filament; nerve; phosphoprotein
F;1-100/Domain: amino-terminal <NTD>
F;101-410/Domain: rod #status predicted <ROD>
F;411-1020/Domain: carboxyl-terminal <CTD>
F;503/Region: 14-residue repeats
F;503,511,518,526,532,540,546,552,560,566,574,580,586,594,600,606,614,620,628,634,640,64
(covalent) #status predicted
F;732,768/Binding site: phosphate (Thr) (covalent) #status predicted

Qy   Query Match
      Best Local Similarity   100.0%; Score 89; DB 1; Length 1020;
      Matches   18; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

         1 AKSPVKEEAKSPEKAKSP 18
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Db   694 AKSPVKEEAKSPEKAKSP 711

RESULT 5
S02003
neurofilament triplet H protein - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 13-Aug-1999
C;Accession: S02003
R;Breen, K.C.; Robinson, P.A.; Wion, D.; Anderton, B.H.
FEBS Lett. 241, 213-218, 1988
A;Title: Partial sequence of the rat heavy neurofilament polypeptide (NF-H). Identificat
A;Reference number: S02003; MUID:89065087; PMID:3143606
A;Accession: S02003
A;Molecule type: mRNA
A;Residues: 1-854 <BRB>
A;Cross-references: EMBL:X13804; NID:g57828; PIDN:CAA32038.1; PID:g57829
C;Superfamily: neurofilament triplet H protein
C;Keywords: coiled coil

Qy   Query Match
      Best Local Similarity   85.4%; Score 76; DB 2; Length 854;
      Matches   18; Conservative   0; Mismatches   0; Indels   6; Gaps   1;

         1 AKSPVKE------EAKSPEKAKSP 18
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Db   525 AKSPVKEGAKSLAEAKSPEKAKSP 548

RESULT 6
A37221
neurofilament triplet H protein - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Dec-1999
C;Accession: A37221
R;Chin, S.S.M.; Liem, R.K.H.
J. Neurosci. 10, 3714-3726, 1990
A;Title: Transfected rat high-molecular-weight neurofilament (NF-H) coassembles with vim
A;Reference number: A37221; MUID:91038277; PMID:2230956
A;Accession: A37221
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-1072 <CHI>
A;Cross-references: GB:Af031879; NID:g2642597; PIDN:AAB87068.1; PID:g2642598
R;Robinson, P.A.; Wion, D.; Anderton, B.H.
FEBS Lett. 209, 203-205, 1986
A;Title: Isolation of a cDNA for the rat heavy neurofilament polypeptide (NF-H).
A;Reference number: A25649; MUID:87080760; PMID:2878828
A;Accession: A25649
A;Molecule type: mRNA
A;Residues: 230-318;472-542 <ROB>
A;Cross-references: GB:M37227
R;Dautigny, A.; Pham-Dinh, D.; Roussel, C.; Felix, J.M.; Nussbaum, J.L.; Jolles, P.
Biochem. Biophys. Res. Commun. 154, 1099-1106, 1988
A;Title: The large neurofilament subunit (NF-H) of the rat: cDNA cloning and in situ det
A;Reference number: A30796; MUID:88309090; PMID:2457365
A;Accession: A30796
A;Molecule type: mRNA
A;Residues: 266-421,'T',423-427,'V',429-542,'V',556-566,'E',568-613,'A',615-725,'S',727-
A;Cross-references: GB:M21964; NID:g205685; PIDN:AAA41695.1; PID:g205686
R;Lieberburg, I.; Spinner, N.; Snyder, S.; Anderson, J.; Goldgaber, D.; Smulowitz, M.; C
Proc. Natl. Acad. Sci. U.S.A. 86, 2463-2467, 1989
A;Title: Cloning of a cDNA encoding the rat high molecular weight neurofilament peptide
22.
A;Reference number: A32757; MUID:89184647; PMID:2928342
A;Accession: A32757
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 55-566,'E',568-967,'V',969-997,'GST',1001-1022,'E',1024-1072 <LIE>
A;Cross-references: GB:J04517; NID:g205679; PIDN:AAA41692.1; PID:g205680
C;Superfamily: neurofilament triplet H protein
C;Keywords: coiled coil; heterotrimer; intermediate filament; nerve; phosphoprotein

Qy   Query Match
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      Matches   18; Conservative   0; Mismatches   0; Indels   6; Gaps   1;

         1 AKSPVKE------EAKSPEKAKSP 18

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OM protein - protein search, using sw model

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                    GenCore version 5.1.6

Run on:             May 25, 2004, 11:14:43 ; Search time 42 Seconds
                                               (without alignments)
                                               119.538 Million cell updates/sec

Sequence:           1 AKSPVKEEAKSPEKAKSP 18
Title:              US-09-847-586-77
Perfect score:      89
Scoring table:      BLOSUM62
                    Gapop 10.0 , Gapext 0.5
Searched:           1149313 seqs, 278921704 residues
Total number of hits satisfying chosen parameters:    1149313

Post-processing:    Minimum Match 0%
Minimum DB seq length: 0
Maximum DB seq length: 200000000

Database :          Published Applications AA:*
                    Listing first 45 summaries
                    1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
                    2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
                    3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
                    4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
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                    6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
                    7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
                    8: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
                    9: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
                    10: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
                    11: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
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                    15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
                    16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
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                    18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*
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SUMMARIES

Result No.	Score	% Query Match	Length	DB ID	Description
1	89	100.0	18	10	US-09-847-586-13	Sequence 13, Appl
2	89	100.0	18	10	US-09-847-586-71	Sequence 71, Appl
3	89	100.0	18	10	US-09-847-586-72	Sequence 72, Appl
4	89	100.0	18	10	US-09-847-586-73	Sequence 73, Appl
5	89	100.0	18	10	US-09-847-586-74	Sequence 74, Appl
6	89	100.0	18	10	US-09-847-586-75	Sequence 75, Appl
7	89	100.0	18	10	US-09-847-586-76	Sequence 76, Appl
8	89	100.0	18	10	US-09-847-586-77	Sequence 77, Appl
9	89	100.0	19	10	US-09-847-586-78	Sequence 78, Appl
10	89	100.0	617	10	US-09-854-761-36182	Sequence 36182, A
11	89	100.0	617	14	US-10-029-386-32114	Sequence 32114, A
12	89	88.8	18	10	US-09-847-586-12	Sequence 12, Appl
13	79	88.8	18	10	US-09-847-586-63	Sequence 63, Appl
14	79	88.8	18	10	US-09-847-586-64	Sequence 64, Appl
15	79	88.8	18	10	US-09-847-586-65	Sequence 65, Appl
16	79	88.8	18	10	US-09-847-586-66	Sequence 66, Appl
17	79	88.8	18	10	US-09-847-586-67	Sequence 67, Appl
18	79	88.8	18	10	US-09-847-586-68	Sequence 68, Appl
19	79	88.8	19	10	US-09-847-586-69	Sequence 69, Appl
20	79	88.8	19	10	US-09-847-586-70	Sequence 70, Appl
21	65	73.0	16	10	US-09-847-586-10	Sequence 10, Appl
22	65	73.0	16	10	US-09-847-586-47	Sequence 47, Appl
23	65	73.0	16	10	US-09-847-586-48	Sequence 48, Appl
24	65	73.0	16	10	US-09-847-586-49	Sequence 49, Appl
25	65	73.0	16	10	US-09-847-586-50	Sequence 50, Appl
26	65	73.0	17	10	US-09-847-586-51	Sequence 51, Appl
27	65	73.0	16	10	US-09-847-586-52	Sequence 52, Appl
28	65	73.0	16	10	US-09-847-586-53	Sequence 53, Appl
29	64	71.9	16	10	US-09-847-586-54	Sequence 54, Appl
30	64	71.9	16	10	US-09-847-586-7	Sequence 7, Appl
31	64	71.9	16	10	US-09-847-586-22	Sequence 22, Appl
32	64	71.9	16	10	US-09-847-586-23	Sequence 23, Appl
33	64	71.9	16	10	US-09-847-586-24	Sequence 24, Appl
34	64	71.9	16	10	US-09-847-586-25	Sequence 25, Appl
35	64	71.9	16	10	US-09-847-586-26	Sequence 26, Appl
36	64	71.9	16	10	US-09-847-586-27	Sequence 27, Appl
37	64	71.9	16	10	US-09-847-586-28	Sequence 28, Appl
38	64	71.9	17	10	US-09-847-586-29	Sequence 29, Appl
39	59	66.3	16	10	US-09-847-586-8	Sequence 8, Appl
40	59	66.3	16	10	US-09-847-586-11	Sequence 11, Appl
41	59	66.3	18	10	US-09-847-586-30	Sequence 30, Appl
42	59	66.3	18	10	US-09-847-586-31	Sequence 31, Appl
43	59	66.3	18	10	US-09-847-586-32	Sequence 32, Appl
44	59	66.3	18	10	US-09-847-586-33	Sequence 33, Appl
45	59	66.3	18	10	US-09-847-586-34	Sequence 34, Appl

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

ALIGNMENTS

```
RESULT 1
US-09-847-586-13
Sequence 13, Application US/09847586
Publication No. US20030148404A1
; GENERAL INFORMATION:
; APPLICANT: Michaelson
; TITLE OF INVENTION: Peptides and substances, methods and devices using same
; TITLE OF INVENTION: for diagnosing and treating neurodegenerative disorders
; FILE REFERENCE: 01/21573
; CURRENT APPLICATION NUMBER: US/09/847,586
; CURRENT FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: PCT IL00/00509
; PRIOR FILING DATE: 2000-08-27
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 13
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:synthetic
; OTHER INFORMATION: peptide
US-09-847-586-13

  Query Match             100.0%;  Score 89;  DB 10;  Length 18;
  Best Local Similarity   100.0%;
  Matches   18;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy          1 AKSPVKEEAKSPEKAKSP 18
              ||||||||||||||||||
Db          1 AKSPVKEEAKSPEKAKSP 18


RESULT 2
US-09-847-586-71
Sequence 71, Application US/09847586
Publication No. US20030148404A1
; GENERAL INFORMATION:
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APPLICANT: Michaelson
TITLE OF INVENTION: Peptides and substances, methods and devices using same
TITLE OF INVENTION: for diagnosing and treating neurodegenerative disorders
FILE REFERENCE: 01/21573
CURRENT APPLICATION NUMBER: US/09/847,586
CURRENT FILING DATE: 2001-05-03
PRIOR APPLICATION NUMBER: PCT IL00/00509
PRIOR FILING DATE: 2000-08-27
NUMBER OF SEQ ID NOS: 79
SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 71
LENGTH: 18
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence
FEATURE:
OTHER INFORMATION: peptide
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (3)
OTHER INFORMATION: PHOSPHORYLATION
US-09-847-586-71

Query Match   100.0%; Score 89; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.5e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    1 AKSPVKEEAKSPEKAKSP 18
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Db    1 AKSPVKEEAKSPEKAKSP 18
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RESULT 3
US-09-847-586-72
Sequence 72, Application US/09847586
Publication No. US20030148404A1
GENERAL INFORMATION:
APPLICANT: Michaelson
TITLE OF INVENTION: Peptides and substances, methods and devices using same
TITLE OF INVENTION: for diagnosing and treating neurodegenerative disorders
FILE REFERENCE: 01/21573
CURRENT APPLICATION NUMBER: US/09/847,586
CURRENT FILING DATE: 2001-05-03
PRIOR APPLICATION NUMBER: PCT IL00/00509
PRIOR FILING DATE: 2000-08-27
NUMBER OF SEQ ID NOS: 79
SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 72
LENGTH: 18
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:synthetic
FEATURE:
OTHER INFORMATION: peptide
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (11)
OTHER INFORMATION: PHOSPHORYLATION
US-09-847-586-72

Query Match   100.0%; Score 89; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.5e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    1 AKSPVKEEAKSPEKAKSP 18
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Db    1 AKSPVKEEAKSPEKAKSP 18
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RESULT 4
US-09-847-586-73
Sequence 73, Application US/09847586
Publication No. US20030148404A1

GENERAL INFORMATION:
APPLICANT: Michaelson
TITLE OF INVENTION: Peptides and substances, methods and devices using same
TITLE OF INVENTION: for diagnosing and treating neurodegenerative disorders
FILE REFERENCE: 01/21573
CURRENT APPLICATION NUMBER: US/09/847,586
CURRENT FILING DATE: 2001-05-03
PRIOR APPLICATION NUMBER: PCT IL00/00509
PRIOR FILING DATE: 2000-08-27
NUMBER OF SEQ ID NOS: 79
SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 73
LENGTH: 18
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:synthetic
FEATURE:
OTHER INFORMATION: peptide
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (17)
OTHER INFORMATION: PHOSPHORYLATION
US-09-847-586-73

Query Match   100.0%; Score 89; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.5e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    1 AKSPVKEEAKSPEKAKSP 18
        ||||||||||||||||||
Db    1 AKSPVKEEAKSPEKAKSP 18
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RESULT 5
US-09-847-586-74
Sequence 74, Application US/09847586
Publication No. US20030148404A1
GENERAL INFORMATION:
APPLICANT: Michaelson
TITLE OF INVENTION: Peptides and substances, methods and devices using same
TITLE OF INVENTION: for diagnosing and treating neurodegenerative disorders
FILE REFERENCE: 01/21573
CURRENT APPLICATION NUMBER: US/09/847,586
CURRENT FILING DATE: 2001-05-03
PRIOR APPLICATION NUMBER: PCT IL00/00509
PRIOR FILING DATE: 2000-08-27
NUMBER OF SEQ ID NOS: 79
SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 74
LENGTH: 18
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:synthetic
FEATURE:
OTHER INFORMATION: peptide
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (11)
OTHER INFORMATION: PHOSPHORYLATION
US-09-847-586-74

Query Match   100.0%; Score 89; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.5e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    1 AKSPVKEEAKSPEKAKSP 18
        ||||||||||||||||||
Db    1 AKSPVKEEAKSPEKAKSP 18
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OM protein - protein search, using sw model

Copyright (c) 1993 - 2004 Compugen Ltd.
GenCore version 5.1.6

Run on: May 25, 2004, 11:12:23 ; Search time 23 Seconds
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Title: US-09-847-586-77
Perfect score: 89
Sequence: 1 AKSPVKEEAKSPEKAKSP 18

Scoring table: BLOSUM62
                  Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

Database :   Issued_Patents_AA:*
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                  4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
                  5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
                  6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	59.5	66.9	160	2	US-08-726-306A-68	Sequence 68, Appl
2	51.5	57.9	35	3	US-08-995-172-18	Sequence 18, Appl
3	48.5	54.5	26	2	US-08-894-339-6	Sequence 6, Appl
4	48.5	54.5	26	3	US-09-306-044-6	Sequence 6, Appl
5	48.5	54.5	218	3	US-10-041-889-4	Sequence 4, Appl
6	48.5	54.5	218	4	US-08-837-058-4	Sequence 4, Appl
7	48.5	54.5	218	4	US-09-417-264-4	Sequence 4, Appl
8	48.5	54.5	61	1	US-08-346-849-17	Sequence 17, Appl
9	48	53.9	61	2	US-08-293-284A-17	Sequence 17, Appl
10	48	53.9	61	4	US-08-898-300-17	Sequence 17, Appl
11	48	53.9	116	3	US-09-041-889-38	Sequence 38, Appl
12	48	53.9	116	3	US-09-417-264-38	Sequence 38, Appl
13	48	53.9	158	4	US-09-041-889-40	Sequence 40, Appl
14	48	53.9	158	4	US-09-417-264-40	Sequence 40, Appl
15	48	53.9	222	3	US-10-041-889-3	Sequence 3, Appl
16	48	53.9	222	3	US-08-837-058-3	Sequence 3, Appl
17	48	53.9	222	4	US-09-417-264-3	Sequence 3, Appl
18	48	53.9	226	3	US-08-468-577B-17	Sequence 17, Appl
19	48	53.9	226	4	US-08-468-579B-17	Sequence 17, Appl
20	48	53.9	712	2	US-09-041-889-32	Sequence 32, Appl
21	48	53.9	712	2	US-08-468-577B-17	Sequence 17, Appl
22	48	53.9	712	3	US-08-468-577B-17	Sequence 17, Appl
23	48	53.9	712	3	US-08-346-849-16	Sequence 16, Appl
24	47.5	53.4	60	2	US-08-293-284A-16	Sequence 16, Appl
25	47.5	53.4	60	4	US-08-898-300-16	Sequence 16, Appl
26	47.5	53.2	30	4	US-08-995-172-11	Sequence 11, Appl
27	46.5	52.2	33	3	US-08-839-624-23	Sequence 23, Appl
28	46.5	52.2	33	4	US-09-150-812-23	Sequence 23, Appl
29	46.5	52.2	60	2	US-08-769-211-2	Sequence 2, Appl
30	46.5	52.2	61	3	US-08-995-172-6	Sequence 6, Appl
31	46.5	52.2	61	3	US-08-995-172-7	Sequence 7, Appl
32	46.5	52.2	113	3	US-09-041-889-14	Sequence 14, Appl
33	46.5	52.2	113	3	US-08-837-058-14	Sequence 14, Appl
34	46.5	52.2	113	3	US-09-417-264-14	Sequence 14, Appl
35	46.5	52.2	147	3	US-09-041-889-13	Sequence 13, Appl
36	46.5	52.2	147	3	US-08-837-058-13	Sequence 13, Appl
37	46.5	52.2	147	4	US-09-417-264-13	Sequence 13, Appl
38	46.5	52.2	220	3	US-09-041-889-2	Sequence 2, Appl
39	46.5	52.2	220	3	US-08-894-339-9	Sequence 9, Appl
40	46.5	52.2	220	3	US-09-417-264-2	Sequence 2, Appl
41	46.5	51.1	26	2	US-08-894-339-9	Sequence 9, Appl
42	45.5	51.1	26	2	US-09-306-044-9	Sequence 9, Appl
43	45.5	50.6	194	4	US-09-125-619-28	Sequence 28, Appl
44	45.5	50.6	212	4	US-09-125-619-48	Sequence 48, Appl
45	46.5	50.6	214	4	US-09-125-619-35	Sequence 35, Appl

ALIGNMENTS

RESULT 1
US-08-726-306A-68

; Sequence 68, Application US/08726306A
; Patent No. 5958684
; GENERAL INFORMATION:
; APPLICANT: van Leeuwen, Frederik Willem
; APPLICANT: Burbach, Johannes Peter Henri
; APPLICANT: Grosveld, Franklin G.
; TITLE OF INVENTION: DIAGNOSIS METHOD AND REAGENTS
; NUMBER OF SEQUENCES: 189
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Witcoff, Ltd.
; STREET: 1 Financial Center
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/726,306A
; FILING DATE: 02-Oct-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 95/20080.4
; FILING DATE: 02-Oct-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/009,832
; FILING DATE: 01-Jan-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams, Ph.D., Kathleen M.
; REGISTRATION NUMBER: 34,380
; REFERENCE/DOCKET NUMBER: 96,048-A (3255/00784)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 345-9100
; TELEFAX: (617) 345-9111
; INFORMATION FOR SEQ ID NO: 68:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 160 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-726-306A-68

Query Match   66.9%; Score 59.5; DB 2; Length 160;
Best Local Similarity 58.3%; Pred. No. 0.17;
Matches   14; Conservative   2; Mismatches   1; Indels   7; Gaps   1;

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Db  131 KSPVEEKGKSPVSKSPVEEKAKSP 154
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RESULT 2
US-08-995-172-18
Sequence 18, Application US/08995172B
Patent No. 6218112
GENERAL INFORMATION:
APPLICANT: Thatcher, David R
APPLICANT: Wilks, Paula E
TITLE OF INVENTION: Optimization of Gene Delivery and Gene Delivery Systems
FILE REFERENCE: CAC00026
CURRENT APPLICATION NUMBER: US/08/995,172B
CURRENT FILING DATE: 1997-12-22
EARLIER APPLICATION NUMBER: 60/033,908
EARLIER FILING DATE: 1996-12-23
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 18
LENGTH: 35
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: UNSURE
LOCATION: (35)
OTHER INFORMATION: Xaa is Cys with Acm sidechain
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Peptide

Query Match   57.9%; Score 51.5; DB 3; Length 35;
Best Local Similarity   44.8%; Pred No.0.49;
Matches 13; Conservative 2; Mismatches 3; Indels 11; Gaps 1;

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Qy  1 AKSPVKEEA----------KSPEKAKSP 18
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Db  3 AKSPAKAKAVKPKAAKPKKSPKKAKKP  31
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RESULT 3
US-08-894-339-6
Sequence 6, Application US/0894339
Patent No. 594540O
GENERAL INFORMATION:
APPLICANT: SHERMAN, Daniel
APPLICANT: BYK, Gerardo
APPLICANT: SCHWARTZ, Bertrand
TITLE OF INVENTION: NUCLEIC ACID-CONTAINING COMPOSITION,
TITLE OF INVENTION: PREPARATION AND USE THEREOF
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, Mailstop 3C43
CITY: Collegeville
STATE: PA
COUNTRY: USA
ZIP: 19426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/894,339
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 95/01865
FILING DATE: 17-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR96/00248
FILING DATE: 15-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Savitzky Esq., Martin F.
REGISTRATION NUMBER: 29,699
REFERENCE/DOCKET NUMBER: ST95012-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 454-3816
TELEFAX: (610) 454-3808
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-894-339-6

Query Match   54.5%; Score 48.5; DB 2; Length 26;
Best Local Similarity   63.2%; Pred. No.0.97;
Matches 12; Conservative 2; Mismatches 2; Indels 4; Gaps 1;

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Qy  1 AKSPVKEEAKSPEKA-KSP 18
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Db  3 AKSPKKAKAAKPKKAPKSP 21
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RESULT 4
US-09-306-044-6
Sequence 6, Application US/09306044
Patent No. 6200956
GENERAL INFORMATION:
APPLICANT: SHERMAN, Daniel
APPLICANT: BYK, Gerardo
APPLICANT: SCHWARTZ, Bertrand
TITLE OF INVENTION: NUCLEIC ACID-CONTAINING COMPOSITION,
TITLE OF INVENTION: PREPARATION AND USE THEREOF
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, Mailstop 3C43
CITY: Collegeville
STATE: PA
COUNTRY: USA
ZIP: 19426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/306,044
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/894,339
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR96/00248
FILING DATE: 15-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Savitzky Esq., Martin F.
REGISTRATION NUMBER: 29,699
REFERENCE/DOCKET NUMBER: ST95012-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 454-3816
TELEFAX: (610) 454-3808
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear

OM protein - protein search, using sw model

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                    GenCore version 5.1.6
              Copyright (c) 1993 - 2004  Compugen Ltd.
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Run on: May 25, 2004, 10:40:52 ; Search time 55 Seconds
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Title: US-09-847-586-77
Perfect score: 89
Sequence: 1 AKSPVKEEAKSPEKAKSP 18
Scoring table: BLOSUM62
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Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
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                 Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | Match DB ID | ID | Description |
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| 2 | 89 | 100.0 | 18 | 5 | ABB09396 | Abb09396 Synthetic |
| 3 | 89 | 100.0 | 18 | 5 | ABB09393 | Abb09393 Synthetic |
| 4 | 89 | 100.0 | 18 | 5 | ABB09395 | Abb09395 Synthetic |
| 5 | 89 | 100.0 | 18 | 5 | ABB09390 | Abb09390 Synthetic |
| 6 | 89 | 100.0 | 18 | 5 | ABB09394 | Abb09394 Synthetic |
| 7 | 89 | 100.0 | 18 | 5 | ABB09389 | Abb09389 Synthetic |
| 8 | 89 | 100.0 | 18 | 5 | ABB09391 | Abb09391 Synthetic |
| 9 | 89 | 100.0 | 19 | 5 | ABB09397 | Abb09397 Synthetic |
| 10 | 89 | 100.0 | 617 | 4 | AAM16458 | Aam16458 Peptide # |
| 11 | 89 | 100.0 | 617 | 4 | ABB35445 | Abb35445 Peptide # |
| 12 | 89 | 100.0 | 617 | 4 | ABB20884 | Abb20884 Protein # |
| 13 | 89 | 100.0 | 617 | 4 | AAM56269 | Aam56269 Human bra |
| 14 | 89 | 100.0 | 617 | 4 | ABG50305 | Abg50305 Human liv |
| 15 | 89 | 100.0 | 617 | 4 | AAM04187 | Aam04187 Peptide # |
| 16 | 89 | 100.0 | 1020 | 7 | ADE63408 | Ade63408 Human Pro |
| 17 | 89 | 100.0 | 1020 | 7 | ADE58910 | Ade58910 Human Pro |
| 18 | 89 | 100.0 | 1026 | 7 | AAM78825 | Aam78825 Human pro |
| 19 | 89 | 100.0 | 1033 | 4 | AAM79809 | Aam79809 Human pro |
| 20 | 79 | 88.8 | 18 | 5 | ABB09382 | Abb09382 Synthetic |
| 21 | 79 | 88.8 | 18 | 5 | ABB09383 | Abb09383 Synthetic |
| 22 | 79 | 88.8 | 18 | 5 | ABB09387 | Abb09387 Synthetic |
| 23 | 79 | 88.8 | 18 | 5 | ABB09385 | Abb09385 Synthetic |
| 24 | 79 | 88.8 | 18 | 5 | ABB09384 | Abb09384 Synthetic |
| 25 | 79 | 88.8 | 18 | 5 | ABB09381 | Abb09381 Synthetic |
| 26 | 79 | 88.8 | 18 | 5 | ABB09386 | Abb09386 Synthetic |
| 27 | 79 | 88.8 | 18 | 5 | ABB09380 | Abb09380 Synthetic |
| 28 | 79 | 88.8 | 19 | 5 | ABB09388 | Abb09388 Synthetic |
| 29 | 76 | 85.4 | 364 | 4 | ABU52998 | Abu52998 Human tes |
| 30 | 76 | 85.4 | 373 | 4 | ABU52996 | Abu52996 Human tes |
| 31 | 76 | 85.4 | 530 | 4 | ABU52995 | Abu52995 Human tes |
| 32 | 76 | 85.4 | 622 | 4 | ABU52993 | Abu52993 Human tes |
| 33 | 76 | 85.4 | 628 | 4 | ABU52994 | Abu52994 Human tes |
| 34 | 76 | 85.4 | 831 | 7 | ADE63406 | Ade63406 Rat Prote |
| 35 | 76 | 85.4 | 831 | 7 | ADE58908 | Ade58908 Rat Prote |
| 36 | 76 | 85.4 | 831 | 7 | ADD44632 | Add44632 Rat Prote |
| 37 | 76 | 85.4 | 1072 | 4 | ABB57023 | Abb57023 Mouse isc |
| 38 | 75 | 84.3 | 420 | 4 | ABU52997 | Abu52997 Human tes |
| 39 | 65 | 73.0 | 16 | 5 | ABB09369 | Abb09369 Synthetic |
| 40 | 65 | 73.0 | 16 | 5 | ABB09362 | Abb09362 Synthetic |
| 41 | 65 | 73.0 | 16 | 5 | ABB09363 | Abb09363 Synthetic |
| 42 | 65 | 73.0 | 16 | 5 | ABB09366 | Abb09366 Synthetic |
| 43 | 65 | 73.0 | 16 | 5 | ABB09367 | Abb09367 Synthetic |
| 44 | 65 | 73.0 | 16 | 5 | ABB09365 | Abb09365 Synthetic |
| 45 | 65 | 73.0 | 16 | 5 | ABB09364 | Abb09364 Synthetic |

ALIGNMENTS

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RESULT 1
ABB09392
ID   ABB09392 standard; peptide; 18 AA.
XX
AC   ABB09392;
XX
DT   01-JUL-2002  (first entry)
XX
DE   Synthetic neurofilament peptide 8R.
XX
KW   NF-H; neurodegenerative disorder; immunogenic epitope; nootropic;
KW   neuroprotective; antiparkinsonian; cerebroprotective; vasotropic;
KW   Alzheimer's disease; multi-infarct dementia; Pick's disease;
KW   frontotemporal dementia; dementia pugilistica; vascular dementia;
KW   Parkinson's disease; Gerstmann-Straussler-Scheinker disease;
KW   multiple sclerosis; Amyotrophic lateral sclerosis;
KW   transient ischaemic attack; stroke; NF-M; Tau; B-amyloid protein.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   17
FT                   /note= "phosphorylated residue"
XX
PN   WO200115655-A2.
XX
PD   08-MAR-2001.
XX
PF   27-AUG-2000; 2000WO-IL000509.
XX
PR   31-AUG-1999;   99US-00386347.
PR   27-JUL-2000; 2000US-0221150P.
XX
PA   (UYRA-) UNIV RAMOT APPLIED RES & IND DEV LTD.
XX
PI   Michaelson DM;
XX
DR   WPI; 2002-179260/23.
XX
PT   identifying existence, non-existence, type or state of neurodegenerative
PT   disorder, by reacting with serum a peptide derived from protein
PT   associated with the disorder, to which antibody is produced at onset of
PT   disorder.
XX
PS   Claim 54; Page 43; 117pp; English.
XX
CC   The invention relates to identifying existence, non-existence, type or
CC   state of neurodegenerative disorder (ND) in individual, involving
```

```
CC   immunoreacting with serum derived from an individual, a peptide
CC   representing an epitope derived from endogenous protein to which an
CC   antibody (Ab) is produced in vivo at onset or during progression of ND,
CC   where Ab immunobinds with the peptide and detecting presence, absence or
CC   degree of immunobinding. Activity of the immunogenic peptides of the
CC   invention may be described as, nootropic, neuroprotective and
CC   antiparkinsonian, cerebroprotective and vasotropic. The peptides of the
CC   invention are useful for identifying existence, non-existence, type or
CC   state of ND in an individual, where ND is associated with progressive
CC   loss of cognitive functions or motoric functions, or progressive loss of
CC   control of motoric functions. Such diseases include; Alzheimer's disease,
CC   Multi-infarct dementia (MID), Pick's disease, frontotemporal dementias,
CC   dementia pugilistica, vascular dementia, Parkinson's disease, Gerstmann-
CC   Strausler-Scheinker disease with tangles, multiple sclerosis,
CC   Amyotrophic lateral sclerosis (ALS), transient ischaemic attack (TIA) and
CC   stroke. In a preferred embodiment of the present invention, the
CC   endogenous protein is selected from the group consisting of NF-H, NF-M,
CC   Tau and B-amyloid protein. The current sequence represents a synthetic
CC   neurofilament peptide derived from the carboxy terminal of NF-H, for use
CC   as an immunogenic epitope. From each of the peptides represented in
CC   records ABB09325, ABB09334, ABB09343, ABB09353, ABB09362, ABB09371,
CC   ABB09380 AND ABB09390, can be generated 8 peptides in different states of
CC   phosphorylation, giving a total of 64 peptides (see ABB09325-ABB09397)
CC   covering all possible states of phosphorylation of the NF-H carboxy
CC   terminal domain
XX
SQ   Sequence 18 AA;

  Query Match          100.0%;  Score 89;  DB 5;  Length 18;
  Best Local Similarity  100.0%;  Pred. No. 3.9e-06;
  Matches   18;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy          1 AKSPVKEEAKSPEKAKSP 18
              ||||||||||||||||||
Db          1 AKSPVKEEAKSPEKAKSP 18

RESULT 2
ID   ABB09396 standard; peptide; 18 AA.
XX
AC   ABB09396;
XX
DT   01-JUL-2002 (first entry)
XX
DE   Synthetic neurofilament peptide 8LMR.
XX
KW   NF-H; neurodegenerative disorder; immunogenic epitope; nootropic;
KW   neuroprotective; antiparkinsonian; cerebroprotective; vasotropic;
KW   Alzheimer's disease; multi-infarct dementia; Pick's disease;
KW   frontotemporal dementia; dementia pugilistica; vascular dementia;
KW   Parkinson's disease; Gerstmann-Strausler-Scheinker disease;
KW   multiple sclerosis; Amyotrophic lateral sclerosis;
KW   transient ischaemic attack; stroke; NF-M; Tau; B-amyloid protein.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
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FT   Modified-site   3
FT                   /note= "phosphorylated residue"
FT   Modified-site   11
FT                   /note= "phosphorylated residue"
FT   Modified-site   17
FT                   /note= "phosphorylated residue"
XX
PN   WO200115655-A2.
XX
PD   08-MAR-2001.
XX
PF   27-AUG-2000; 2000WO-IL000509.
XX
PR   31-AUG-1999; 99US-00386347.
PR   27-JUL-2000; 2000US-0221150P.
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XX
PA   (UYRA-) UNIV RAWOT APPLIED RES & IND DEV LTD.
XX
PI   Michaelson DM;
XX
DR   WPI; 2002-179260/23.
XX
PT   Identifying existence, non-existence, type or state of neurodegenerative
PT   disorder, by reacting with serum a peptide derived from protein
PT   associated with the disorder, to which antibody is produced at onset of
PT   disorder.
XX
PS   Example 1; Page 43; 117pp; English.
XX
CC   The invention relates to identifying existence, non-existence, type or
CC   state of neurodegenerative disorder (ND) in individual, involving
CC   immunoreacting with serum derived from an individual, a peptide
CC   representing an epitope derived from endogenous protein to which an
CC   antibody (Ab) is produced in vivo at onset or during progression of ND,
CC   where Ab immunobinds with the peptide and detecting presence, absence or
CC   degree of immunobinding. Activity of the immunogenic peptides of the
CC   invention may be described as, nootropic, neuroprotective and
CC   antiparkinsonian, cerebroprotective and vasotropic. The peptides of the
CC   invention are useful for identifying existence, non-existence, type or
CC   state of ND in an individual, where ND is associated with progressive
CC   loss of cognitive functions or motoric functions, or progressive loss of
CC   control of motoric functions. Such diseases include; Alzheimer's disease,
CC   Multi-infarct dementia (MID), Pick's disease, frontotemporal dementias,
CC   dementia pugilistica, vascular dementia, Parkinson's disease, Gerstmann-
CC   Strausler-Scheinker disease with tangles, multiple sclerosis,
CC   Amyotrophic lateral sclerosis (ALS), transient ischaemic attack (TIA) and
CC   stroke. In a preferred embodiment of the present invention, the
CC   endogenous protein is selected from the group consisting of NF-H, NF-M,
CC   Tau and B-amyloid protein. The current sequence represents a synthetic
CC   neurofilament peptide derived from the carboxy terminal of NF-H, for use
CC   as an immunogenic epitope. From each of the peptides represented in
CC   records ABB09325, ABB09334, ABB09343, ABB09353, ABB09362, ABB09371,
CC   ABB09380 AND ABB09390, can be generated 8 peptides in different states of
CC   phosphorylation, giving a total of 64 peptides (see ABB09325-ABB09397)
CC   covering all possible states of phosphorylation of the NF-H carboxy
CC   terminal domain
XX
SQ   Sequence 18 AA;

  Query Match          100.0%;  Score 89;  DB 5;  Length 18;
  Best Local Similarity  100.0%;  Pred. No. 3.9e-06;
  Matches   18;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy          1 AKSPVKEEAKSPEKAKSP 18
              ||||||||||||||||||
Db          1 AKSPVKEEAKSPEKAKSP 18

RESULT 3
ID   ABB09393 standard; peptide; 18 AA.
XX
AC   ABB09393;
XX
DT   01-JUL-2002 (first entry)
XX
DE   Synthetic neurofilament peptide 8LM.
XX
KW   NF-H; neurodegenerative disorder; immunogenic epitope; nootropic;
KW   neuroprotective; antiparkinsonian; cerebroprotective; vasotropic;
KW   Alzheimer's disease; multi-infarct dementia; Pick's disease;
KW   frontotemporal dementia; dementia pugilistica; vascular dementia;
KW   Parkinson's disease; Gerstmann-Strausler-Scheinker disease;
KW   multiple sclerosis; Amyotrophic lateral sclerosis;
KW   transient ischaemic attack; stroke; NF-M; Tau; B-amyloid protein.
XX
OS   Synthetic.
XX
```

OM protein - protein search, using sw model

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GenCore version 5.1.6

Run on: May 25, 2004, 11:03:57 ; Search time 11 Seconds (without alignments)
     85.206 Million cell updates/sec

Title:
Perfect score: 89
Sequence: 1 AKSPVKEEAKSPEKAKSP 18

Run on: US-09-847-586-77

Post-processing: Minimum Match 0%
     Maximum Match 100%
     Listing first 45 summaries

Scoring table: BLOSUM62
     Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Database :   SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Accession	Description
1	89	100.0	1026	1	NFH_HUMAN	P12036	homo sapien
2	76	85.4	831	1	NFH_RAT	P16884	rattus norv
3	76	85.4	1087	1	NFH_MOUSE	P19246	mus musculu
4	59.5	66.9	915	1	NFM_HUMAN	P07197	homo sapien
5	51.5	57.9	6632	1	UN89_CAEEL	O01761	caenorhabdi
6	51	57.3	1815	1	SHK3_RAT	Q9JLV4	rattus norv
7	50	56.2	810	1	NFM_BOVIN	O77788	bos taurus
8	49	55.1	1113	1	H2B_OIILU	P82887	olisthodisc
9	49	55.1	848	1	NFM_MOUSE	P08553	mus musculu
10	48.5	54.5	218	1	H4_HUMAN	P10412	homo sapien
11	48	53.9	206	1	H1C2_ONCMY	P06350	oncorhynchu
12	48	53.9	216	1	H1C1_XENLA	P15866	xenopus lae
13	48	53.9	217	1	H1_ANAPL	P09426	anas platyr
14	48	53.9	217	1	H1_CHICK	P09987	gallus gall
15	48	53.9	218	1	H101_CHICK	P09984	gallus gall
16	48	53.9	219	1	H110_CHICK	P08286	gallus gall
17	48	53.9	222	1	H1C2_XENLA	P15867	xenopus lae
18	48	53.9	222	1	H15_MOUSE	P43276	mus musculu
19	48	53.9	225	1	H15_HUMAN	P16401	homo sapien
20	48	53.9	225	1	NFM_RAT	P12839	rattus norv
21	48	53.9	857	1	NFM_CHICK	P16053	gallus gall
22	48	53.9	209	1	H1A_XENLA	P06892	xenopus lae
23	47.5	53.4	220	1	H13_MOUSE	P43277	mus musculu
24	47.5	53.4	248	1	H1_PARAN	P02256	parechinus
25	47.5	53.4	205	1	H1E_STRPU	P19375	strongyloce
26	47	52.8	205	1	H1R_CHICK	P08288	gallus gall
27	47	52.8	223	1	H103_CHICK	P08285	gallus gall
28	47	52.8	224	1	H11_CHICK	P08287	gallus gall
29	47	52.8	233	1	H11_GLYBA	P40263	glyptocendi
30	47	52.8	484	1	MEC2_MOUSE	Q9Z226	mus musculu
31	47	52.8	486	1	MEC2_HUMAN	P51608	homo sapien
32	47	52.8	492	1	MEC2_RAT	Q00556	rattus norv
33	46.5	52.2	219	1	H1B_XENLA	P06893	xenopus lae
34	46.5	52.2	220	1	H13_HUMAN	P16402	homo sapien
35	46.5	52.2	238	1	H1_WHEAT	P27806	triticum ae
36	46	51.7	211	1	H12_MOUSE	P15864	mus musculu
37	46	51.7	1007	1	PR4B_MOUSE	Q61136	mus musculu
38	45.5	51.1	194	1	H5B_XENIA	P22845	xenopus lae
39	45.5	51.1	196	1	H5A_XENIA	P22844	xenopus lae
40	45	50.6	559	1	DACA_HUMAN	Q9by19	homo sapien
41	45	50.6	1130	1	YL17_CAEEL	Q11102	caenorhabdi
42	44.5	50.0	159	1	H2A_MAIZE	P40280	zea mays (m
43	44.5	50.0	171	1	H1_ECHGR	P22257	echinolempa
44	44.5	50.0	194	1	H1_SALTR	P02254	salmo trutt
45	44.5	50.0	213	1	H13_RABIT	P02251	oryctolagus

ALIGNMENTS

RESULT 1
NFH_HUMAN

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ID   NFH_HUMAN      STANDARD;      PRT;  1026 AA.
AC   P12036; Q9UJS7; Q9UQ14;
DT   01-OCT-1989 (Rel. 12, Created)
DT   10-OCT-2003 (Rel. 12, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Neurofilament triplet H protein (200 kDa neurofilament protein)
DE   (Neurofilament heavy polypeptide) (NF-H).
GN   NFH OR NFH OR KIAA0845.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=88329981; PubMed=3138108;
RA   Lees J.F., Shneidman P.S., Skuntz S.F., Carden M.J., Lazzarini R.A.;
RT   "The structure and organization of the human heavy neurofilament
RT   subunit (NF-H) and the gene encoding it.";
RL   EMBO J. 7:1947-1955(1988).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99156230; PubMed=10048485;
RA   Nagase T., Ishikawa K.-I., Suyama M., Kikuno R., Hirosawa M.,
RA   Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
RT   "Prediction of the coding sequences of unidentified human genes. XII.
RT   The complete sequences of 100 new cDNA clones from brain which code
RT   for large proteins in vitro.";
RL   DNA Res. 5:355-364(1998).
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Zhu Y., Han Y.;
RT   "Molecular Cloning of human hSTE cDNA.";
RL   Beijing Yi Ke Da Xue Xue Bao 31:531-531(1999).
CC   -!- FUNCTION: Neurofilaments usually contain three intermediate
CC       filament proteins: L, M, and H which are involved in the
CC       maintenance of neuronal caliber. NF-H has an important function in
CC       mature axons that is not subserved by the two smaller NF proteins.
CC   -!- PTM: There are a number of repeats of the tripeptide K-S-P, NFH is
CC       phosphorylated on a number of the serines in this motif. It is
CC       thought that phosphorylation of NFH results in the formation of
CC       interfilament cross bridges that are important in the maintenance
CC       of axonal caliber.
CC   -!- PTM: Phosphorylation seems to play a major role in the functioning
CC       of the larger neurofilament polypeptides (NF-M and NF-H), the
CC       levels of phosphorylation being altered developmentally and
CC       coincident with a change in the neurofilament function.
CC   -!- SIMILARITY: Belongs to the intermediate filament family.
CC   -------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   -----------------------------------------------------------------------
DR   EMBL; X15306; CAA33366.1; -.
DR   EMBL; X15307; CAA33366.1; JOINED.
DR   EMBL; X15308; CAA33366.1; JOINED.
DR   EMBL; X15309; CAA33366.1; JOINED.
DR   EMBL; AF203032; AAF13722.1; -.
DR   EMBL; AB020652; BAA74868.2; -.
DR   PIR; S00979; QPHUH.
DR   Genew; HGNC:7737; NEFH.
DR   MIM; 162230; -.
DR   GO; GO:0005883; C:neurofilament; NAS.
DR   GO; GO:0007399; P:neurogenesis; NAS.
DR   InterPro; IPR001664; IF.
DR   Pfam; PF00038; filament; 1.
DR   PROSITE; PS00226; IF; 1.
KW   Intermediate filament; Coiled coil; Neurone; Phosphorylation; Repeat.
FT   DOMAIN       1    100       HEAD.
FT   DOMAIN     101    413       ROD.
FT   DOMAIN     414   1026       TAIL.
FT   DOMAIN     101    132       COIL 1A.
FT   DOMAIN     133    145       LINKER 1.
FT   DOMAIN     146    244       COIL 1B.
FT   DOMAIN     245    266       LINKER 12.
FT   DOMAIN     267    288       COIL 2A.
FT   DOMAIN     289    292       LINKER 2.
FT   DOMAIN     293    413       COIL 2B.
FT   CONFLICT   651    656       MISSING (IN REF. 1).
FT   CONFLICT   811    811       E -> A (IN REF. 1).
SQ   SEQUENCE 1026 AA; 112478 MW; 0879B6A08D208C17 CRC64;
```

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Query Match     100.0%;  Score 89;  DB 1;  Length 1026;
Best Local Similarity   100.0%;  Pred. No. 4.4e-05;
Matches   18;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy      1 AKSPVKEEAKSPEKAKSP 18
          ||||||||||||||||||
Db    700 AKSPVKEEAKSPEKAKSP 717
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RESULT 2
ID   NFH_RAT     STANDARD;     PRT;   831 AA.
AC   P16884; Q63368;
DT   01-AUG-1990 (Rel. 15, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Neurofilament triplet H protein (200 kDa neurofilament protein)
DE   (Neurofilament heavy polypeptide) (NF-H) (fragment).
GN   NEFH OR NFH.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=89065087; PubMed=3143606;
RA   Breen K.C., Robinson P.A., Wion D., Anderton B.H.;
RT   "Partial sequence of the rat neurofilament polypeptide (NF-H).";
RL   FEBS Lett. 241:213-218(1988).
RN   [2]
RP   SEQUENCE OF 37-831 FROM N.A.
RX   MEDLINE=88309090; PubMed=2457365;
RA   Dautigny A., Pham-Dinh D., Roussel C., Felix J.M., Nussbaum J.L.,
RA   Jolles P.;
RT   "The large neurofilament subunit (NF-H) of the rat: cDNA cloning and
RT   in situ detection.";
RL   Biochem. Biophys. Res. Commun. 154:1099-1106(1988).
RN   [3]
RP   SEQUENCE OF 1-89 AND 243-313 FROM N.A.
```

```
RX   MEDLINE=87080760; PubMed=2878828;
RA   Robinson P.A., Wion D., Anderton B.H.;
RT   "Isolation of a cDNA for the rat heavy neurofilament polypeptide
RT   (NF-H).";
RL   FEBS Lett. 209:203-205 (1986).
RN   [4]
RP   SEQUENCE OF 318-831 FROM N.A.
RX   MEDLINE=89184647; PubMed=2928342;
RA   Lieberburg I., Spinner N., Snyder S., Anderson J., Goldgaber D.,
RA   Smulowitz M., Carroll Z., Emanuel B.S., Breitner J., Rubin L.;
RT   "Cloning of a cDNA encoding the rat high molecular weight
RT   neurofilament peptide (NF-H): developmental and tissue expression in
RT   the rat, and mapping of its human homologue to chromosomes 1 and
RT   22.";
RL   Proc. Natl. Acad. Sci. U.S.A. 86:2463-2467(1989).
CC   -!- FUNCTION: Neurofilaments usually contain three intermediate
CC       filament proteins: L, M, and H which are involved in the
CC       maintenance of neuronal caliber. NF-H has an important function in
CC       mature axons that is not subserved by the two smaller NF proteins.
CC   -!- PTM: There are a number of repeats of the tripeptide K-S-P, NFH is
CC       phosphorylated on a number of the serines in this motif. It is
CC       thought that phosphorylation of NFH results in the formation of
CC       interfilament cross bridges that are important in the maintenance
CC       of axonal caliber.
CC   -!- PTM: Phosphorylation seems to play a major role in the functioning
CC       of the larger neurofilament polypeptides (NF-M and NF-H), the
CC       levels of phosphorylation being altered developmentally and
CC       coincident with a change in the neurofilament function.
CC   -!- SIMILARITY: Belongs to the intermediate filament family.
CC   -!- CAUTION: Ref.1 sequence differs from that shown due to a
CC       frameshift in position 783.
```

```
DR   EMBL; M37227; AAA41693.1; ALT_FRAME.
DR   EMBL; X13804; CAA32038.1; ALT_FRAME.
DR   EMBL; M21964; AAA41695.1; -.
DR   EMBL; J04517; AAA41692.1; -.
DR   PIR; S02003; S02003.
DR   InterPro; IPR001664; IF.
DR   Pfam; PF00038; filament; 1.
DR   PROSITE; PS00226; IF; 1.
KW   Intermediate filament; Coiled coil; Neurone; Phosphorylation; Repeat.
FT   NON_TER      1      1
FT   DOMAIN      51     X 3      AA TANDEM REPEATS OF K-S-P.
FT   DOMAIN     276    641
FT   CONFLICT   164    164       K -> N (IN REF. 1).
FT   CONFLICT   185    185       L -> S (IN REF. 2).
FT   CONFLICT   193    193       L -> T (IN REF. 2).
FT   CONFLICT   199    199       M -> T (IN REF. 2).
FT   CONFLICT   346    346       K -> N (IN REF. 1).
FT   CONFLICT   373    373       A -> V (IN REF. 1 AND 4).
FT   CONFLICT   482    482       A -> V (IN REF. 1 AND 4).
FT   CONFLICT   485    485       G -> E (IN REF. 2).
FT   CONFLICT   570    571       RK -> KE (IN REF. 2 AND 4).
FT   CONFLICT   591    591       P -> T (IN REF. 2 AND 4).
FT   CONFLICT   727    727       A -> V (IN REF. 4).
FT   CONFLICT   757    759       AAP -> GST (IN REF. 4).
FT   CONFLICT   769    769       T -> L (IN REF. 2).
FT   CONFLICT   775    775       R -> P (IN REF. 2 AND 4).
SQ   SEQUENCE 831 AA; 89486 MW; 1B0973C3F13BF768 CRC64;
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Query Match     85.4%;  Score 76;  DB 1;  Length 831;
Best Local Similarity   75.0%;  Pred. No. 0.0025;
Matches   18;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   1;

Qy      1 AKSPVKE--------EAKSPEKAKSP 18
          ||||||         ||||||||||
```